

**IN THE SPECIFICATION:**

At page 17, please amend paragraph [0067] as follows:

Figure 3 is a graphic representation illustrating that Dam regulates *in vivo* induced genes. [b]  $\beta$ -galactosidase expression from *S. typhimurium* *ivi* fusions in Dam<sup>+</sup> and Dam<sup>-</sup> strains grown in LB. The vertical axis shows [b]  $\beta$ -galactosidase activities ( $\mu$ -moles of o-nitrophenol (ONP) formed per minute per A<sub>600</sub> unit per milliliter of cell suspension x 10<sup>3</sup>).

At page 18, please amend paragraph [0068] as follows:

Figure 4 is a graphic representation illustrating that Dam represses PhoP activated genes. [b]  $\beta$ -galactosidase from *S. typhimurium* *ivi* fusions grown in minimal medium. The vertical axis shows [b]  $\beta$ -galactosidase activities ( $\mu$ -moles of o-nitrophenol (ONP) formed per minute per A<sub>600</sub> unit per milliliter of cell suspension x 10<sup>3</sup>). The *Dam* genotype is shown below the horizontal axis, and the *phoP* genotypes is shown as black (PhoP<sup>+</sup>) and gray (PhoP<sup>-</sup>) boxes.

At page 18, please amend paragraph [0070] as follows:

[Figure 6] Figures 6A and 6B are graphs depicting the amount and tissue distribution of *Salmonella* in mice immunized with Dam<sup>-</sup> mutants (solid boxes) or not immunized (open boxes) on day 1 and day 5 respectively. PP, Peyer's patches; MLN, mesenteric lymph nodes; CFU, colony forming units.

At page 18, please amend paragraph [0071] as follows:

[Figure 7] Figures 7A-7D are graphs depicting amount and tissue distribution of *Salmonella* in mice immunized with Dam<sup>-</sup> mutants (solid boxes) or not immunized (open boxes) on days 1, 5, 14 and 28 respectively. PP, Peyer's patches; MLN, mesenteric lymph nodes; CFU, colony forming units.

At pages 67-68, please amend paragraph [00244] as follows:

[0244] All bacterial strains used in this study were derivatives of *S. typhimurium* 14028 (strain 1). Mutant strains were isogenic to wild type and were obtained or constructed as described (*Dam102::Mud-Cm* and *mutS121::Tn10* alleles are in LT2 (strain 7), a highly attenuated (virtually non-pathogenic) strain as shown in Table 2, were obtained from Dr. John Roth (University of Utah) and Dr. Tom Cebula (The Food and Drug Administration), respectively; these alleles (and additional alleles below) were transduced into virulent strain, 14028, constructing strains 2 and 5, respectively. *Dam[Δ]Δ232* (strain 3) was constructed using internal oligonucleotides that serve as PCR primers designed to construct an in-frame 300 bp deletion of defined *Dam* sequence. *dcm1::Km* was constructed according to (Julio, S. M., *et al.*, *Molec. Gen. Genet.*, **258**: 178-181 (1998)); the Km resistance determinant is associated with an internal deletion of >600 bp of *dcm* sequence. The *lrp31::Km* is a null insertion in the *lrp* gene (strain 6). The Dam overproducing strain (strain 4) contains *E. coli* *Dam* on a recombinant plasmid (pTP166) in a wild-type background (Marinus, *et al.*, *Gene*, **28**:123-125 (1984).

At page 70, please amend Table 1 as follows:

**TABLE 1**

Strain *	Genotype	Oral LD <sub>50</sub>	I.P. LD <sub>50</sub> #	Competitive Index (I.P.) <sup>a</sup>
1	"wild type"	>10 <sup>+5</sup>	>10	---
2	<i>dam102::Mud-Cm</i>	>10 <sup>+9</sup>	>10 <sup>+4</sup>	<10 <sup>-4</sup>
3	<i>Dam[Δ]Δ232</i> (non-polar deletion)	>10 <sup>+6</sup>	>10 <sup>+4</sup>	<10 <sup>-4</sup>
4	wild type, (pTP166) (Dam overproducer)	>10 <sup>+8</sup>	>10 <sup>+4</sup>	<10 <sup>-4</sup>
5	<i>mutS121::Tn10</i>	10 <sup>+5</sup>	ND	0.9
6	<i>lrp31::Km</i>	10 <sup>+5</sup>	ND	10.0
7	LT2	ND	2 x 10 <sup>+4</sup>	ND